

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: Jarl Wikberg
 (B) STREET: Trillvaegen 13
 (C) CITY: Umea
 (E) COUNTRY: Sweden
 (F) POSTAL CODE (ZIP): 905 92 Umea

(A) NAME: Vijay Chhajlani
 (B) STREET: Stigbergsvaegen
 (C) CITY: Uppsala
 (E) COUNTRY: Sweden
 (F) POSTAL CODE (ZIP): 752 42 Uppsala

(ii) TITLE OF INVENTION: New polypeptides

(iii) NUMBER OF SEQUENCES: 16

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1270 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 169..1122

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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GGAGAGGGTG TGAGGGCAGA TCTGGGGGTG CCCAGATGGA AGGAGGCAGG CATGGGGGGAC      60
ACCCAAGGCC CCCTGGCAGC ACCATGAACT AAGCAGGACA CCTGGAGGGG AAGAACTGTG      120
GGGACCTGGA GGCCTCCAAC GACTCCTTCC TGCTTCCTGG ACAGGACT ATG GCT GTG      177
                                     Met Ala Val
                                     1

CAG GGA TCC CAG AGA AGA CTT CTG GGC TCC CTC AAC TCC ACC CCC ACA      225
Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser Thr Pro Thr
      5              10              15

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GCC ATC CCC CAG CTG GGG CTG GCT GCC AAC CAG ACA GGA GCC CGG TGC	273
Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly Ala Arg Cys	
20 25 30 35	
CTG GAG GTG TCC ATC TCT GAC GGG CTC TTC CTC AGC CTG GGG CTG GTG	321
Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu Gly Leu Val	
40 45 50	
AGC TTG GTG GAG AAC GCG CTG GTG GTG GCC ACC ATC GCC AAG AAC CGG	369
Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala Lys Asn Arg	
55 60 65	
AAC CTG CAC TCA CCC ATG TAC TGC TTC ATC TGC TGC CTG GCC TTG TCG	417
Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu Ala Leu Ser	
70 75 80	
GAC CTG CTG GTG AGC GGG AGC AAC GTG CTG GAG ACG GCC GTC ATC CTC	465
Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala Val Ile Leu	
85 90 95	
CTG CTG GAG GCC GGT GCA CTG GTG GCC CGG GCT GCG GTG CTG CAG CAG	513
Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val Leu Gln Gln	
100 105 110 115	
CTG GAC AAT GTC ATT GAC GTG ATC ACC TGC AGC TCC ATG CTG TCC AGC	561
Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met Leu Ser Ser	
120 125 130	
CTC TGC TTC CTG GGC GCC ATC GCC GTG GAC CGC TAC ATC TCC ATC TTC	609
Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile Ser Ile Phe	
135 140 145	
TAC GCA CTG CGC TAC CAC AGC ATC GTG ACC CTG CCG CGG GCG CGG CGA	657
Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Arg Arg	
150 155 160	
CGC GTT GCG GCC ATC TGG GTG GCC AGT GTC GTC TTC AGC ACG CTC TTC	705
Arg Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe	
165 170 175	
ATC GCC TAC TAC GAC CAC GTG GCC GTC CTG CTG TGC CTC GTG GTC TTC	753
Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe	
180 185 190 195	
TTC CTG GCT ATG CTG GTG CTC ATG GCC GTG CTG TAC GTC CAC ATG CTG	801
Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu	
200 205 210	
GCC CGG GCC TGC CAG CAC GCC CAG GGC ATC GCC CGG CTC CAC AAG AGG	849
Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg	
215 220 225	
CAG CGC CCG GTC CAC CAG GGC TTT GGC CTT AAA GGC GCT GTC ACC CTC	897
Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu	
230 235 240	

ACC ATC CTG CTG GGC ATT TTC TTC CTC TGC TGG GGC CCC TTC TTC CTG 945
 Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro Phe Phe Leu
 245 250 255

CAT CTC ACA CTC ATC GTC CTC TGC CCC GAG CAC CCC ACG TGC GGC TGC 993
 His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr Cys Gly Cys
 260 265 270 275

ATC TTC AAG AAC TTC AAC CTC TTT CTC GCC CTC ATC ATC TGC AAT GCC 1041
 Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile Cys Asn Ala
 280 285 290

ATC ATC GAC CCC CTC ATC TAC GCC TTC CAC AGC CAG GAG CTC CGC AGG 1089
 Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu Leu Arg Arg
 295 300 305

ACG CTC AAG GAG GTG CTG ACA TGC TCC TGG TGAGCGCGGT GCACGCGCTT 1139
 Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
 310 315

TAAGTGTGCT GGGCAGAGGG AGGTGGTGAT ATTGTGTGGT CTGGTTCCTG TGTGACCCTG 1199

GGCAGTTCCT TACCTCCCTG GTCCCCGTTT GTCAAAGAGG ATGGACTAAA TGATCTCTGA 1259

AAGTGTGAA G 1270

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ala Val Gln Gly Ser Gln Arg Arg Leu Leu Gly Ser Leu Asn Ser
 1 5 10 15

Thr Pro Thr Ala Ile Pro Gln Leu Gly Leu Ala Ala Asn Gln Thr Gly
 20 25 30

Ala Arg Cys Leu Glu Val Ser Ile Ser Asp Gly Leu Phe Leu Ser Leu
 35 40 45

Gly Leu Val Ser Leu Val Glu Asn Ala Leu Val Val Ala Thr Ile Ala
 50 55 60

Lys Asn Arg Asn Leu His Ser Pro Met Tyr Cys Phe Ile Cys Cys Leu
 65 70 75 80

Ala Leu Ser Asp Leu Leu Val Ser Gly Ser Asn Val Leu Glu Thr Ala
 85 90 95

Val Ile Leu Leu Leu Glu Ala Gly Ala Leu Val Ala Arg Ala Ala Val
 100 105 110

98

Leu Gln Gln Leu Asp Asn Val Ile Asp Val Ile Thr Cys Ser Ser Met
 115 120 125
 Leu Ser Ser Leu Cys Phe Leu Gly Ala Ile Ala Val Asp Arg Tyr Ile
 130 135 140
 Ser Ile Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Leu Pro Arg
 145 150 155 160
 Ala Arg Arg Arg Val Ala Ala Ile Trp Val Ala Ser Val Val Phe Ser
 165 170 175
 Thr Leu Phe Ile Ala Tyr Tyr Asp His Val Ala Val Leu Leu Cys Leu
 180 185 190
 Val Val Phe Phe Leu Ala Met Leu Val Leu Met Ala Val Leu Tyr Val
 195 200 205
 His Met Leu Ala Arg Ala Cys Gln His Ala Gln Gly Ile Ala Arg Leu
 210 215 220
 His Lys Arg Gln Arg Pro Val His Gln Gly Phe Gly Leu Lys Gly Ala
 225 230 235 240
 Val Thr Leu Thr Ile Leu Leu Gly Ile Phe Phe Leu Cys Trp Gly Pro
 245 250 255
 Phe Phe Leu His Leu Thr Leu Ile Val Leu Cys Pro Glu His Pro Thr
 260 265 270
 Cys Gly Cys Ile Phe Lys Asn Phe Asn Leu Phe Leu Ala Leu Ile Ile
 275 280 285
 Cys Asn Ala Ile Ile Asp Pro Leu Ile Tyr Ala Phe His Ser Gln Glu
 290 295 300
 Leu Arg Arg Thr Leu Lys Glu Val Leu Thr Cys Ser Trp
 305 310 315

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GGGAATTCTG TGTGTNATCN CNGTGGACCG GTA

33

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GGGGATCCGA AGAAGGGNAA CCAGCAGAGN ATGAA

35

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (PCR-fragment)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTC	TAC	GCA	CTG	CGC	TAC	CAC	AGC	ATC	GTG	ACC	ATG	CGC	CGC	ACT	GTG	48
Phe	Tyr	Ala	Leu	Arg	Tyr	His	Ser	Ile	Val	Thr	Met	Arg	Arg	Thr	Val	
1				5					10					15		
GTG	GTG	CTT	ACG	GTC	ATC	TGG	ACG	TTC	TGC	ACG	GGG	ACT	GGC	ATC	ACC	96
Val	Val	Leu	Thr	Val	Ile	Trp	Thr	Phe	Cys	Thr	Gly	Thr	Gly	Ile	Thr	
		20						25					30			
ATG	GTG	ATC	TTC	TCC	CAT	CAT	GTG	CCC	ACA	GTG	ATC	ACC	TTC	ACG	TCG	144
Met	Val	Ile	Phe	Ser	His	His	Val	Pro	Thr	Val	Ile	Thr	Phe	Thr	Ser	
		35					40					45				
CTG	TTC	CCG	CTG	ATG	CTG	GTC	TTC	ATC	CTG	TGC	CTC	TAT	GTG	CAC	ATG	192
Leu	Phe	Pro	Leu	Met	Leu	Val	Phe	Ile	Leu	Cys	Leu	Tyr	Val	His	Met	
		50				55						60				
TTC	CTG	CTG	GCT	CGA	TCC	CAC	ACC	AGG	AAG	ATC	TCC	ACC	CTC	CCC	AGA	240
Phe	Leu	Leu	Ala	Arg	Ser	His	Thr	Arg	Lys	Ile	Ser	Thr	Leu	Pro	Arg	
	65				70				75				80			
GCC	AAC	ATG	AAA	GGG	GCC	ATC	ACC	CTC	ACC	ATC	CTG	CTG	GGC	ATT		285
Ala	Asn	Met	Lys	Gly	Ala	Ile	Thr	Leu	Thr	Ile	Leu	Leu	Gly	Ile		
			85					90					95			

100

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

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Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Met Arg Arg Thr Val
 1             5             10             15
Val Val Leu Thr Val Ile Trp Thr Phe Cys Thr Gly Thr Gly Ile Thr
      20             25             30
Met Val Ile Phe Ser His His Val Pro Thr Val Ile Thr Phe Thr Ser
      35             40             45
Leu Phe Pro Leu Met Leu Val Phe Ile Leu Cys Leu Tyr Val His Met
      50             55             60
Phe Leu Leu Ala Arg Ser His Thr Arg Lys Ile Ser Thr Leu Pro Arg
      65             70             75             80
Ala Asn Met Lys Gly Ala Ile Thr Leu Thr Ile Leu Leu Gly Ile
      85             90             95

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(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (PCR-fragment)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..306

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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TTC TAC GCA CTG CGC TAC CAC AGC ATC GTG ACG GCG AGG CGC TCA GGG      48
Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Ala Arg Arg Ser Gly
 1             5             10             15

GCC ATC ATC GCC GGC ATC TGG GCT TTC TGC ACG GGC TGC GGC ATT GTC      96
Ala Ile Ile Ala Gly Ile Trp Ala Phe Cys Thr Gly Cys Gly Ile Val
      20             25             30

TTC ATC CTG TAC TCA GAA TCC ACC TAC GTC ATC CTG TGC CTC ATC TCC      144
Phe Ile Leu Tyr Ser Glu Ser Thr Tyr Val Ile Leu Cys Leu Ile Ser
      35             40             45

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101

ATG TTC TTC GCT ATG CTG TTC CTC CTG GTG TCT CTG TAC ATA CAC ATG	192
Met Phe Phe Ala Met Leu Phe Leu Leu Val Ser Leu Tyr Ile His Met	
50 55 60	
TTC CTC CTG GCG CGG ACT CAC GTC AAG CGG ATC GCG CTC TGC CCG GGG	240
Phe Leu Leu Ala Arg Thr His Val Lys Arg Ile Ala Leu Cys Pro Gly	
65 70 75 80	
CCA GCT CTG CGC GGC AGA GGA CCA GCA TGC AGG GGC GCG GTC ACC CTC	288
Pro Ala Leu Arg Gly Arg Gly Pro Ala Cys Arg Gly Ala Val Thr Leu	
85 90 95	
ACC ATC CTG CTG GGC ATT	306
Thr Ile Leu Leu Gly Ile	
100	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Ala Arg Arg Ser Gly	
1 5 10 15	
Ala Ile Ile Ala Gly Ile Trp Ala Phe Cys Thr Gly Cys Gly Ile Val	
20 25 30	
Phe Ile Leu Tyr Ser Glu Ser Thr Tyr Val Ile Leu Cys Leu Ile Ser	
35 40 45	
Met Phe Phe Ala Met Leu Phe Leu Leu Val Ser Leu Tyr Ile His Met	
50 55 60	
Phe Leu Leu Ala Arg Thr His Val Lys Arg Ile Ala Leu Cys Pro Gly	
65 70 75 80	
Pro Ala Leu Arg Gly Arg Gly Pro Ala Cys Arg Gly Ala Val Thr Leu	
85 90 95	
Thr Ile Leu Leu Gly Ile	
100	

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (PCR-fragment)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..312

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TTC TAC GCA CTG CGT TAC CAC AGC ATC GTG ACC GTG CGG CGG GCC CTC	48
Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Val Arg Arg Ala Leu	
1 5 10 15	
ACC TTG ATC GTG GCC ATC TGG GTC TGC TGC GGC GTC TGT GGC GTG GTG	96
Thr Leu Ile Val Ala Ile Trp Val Cys Cys Gly Val Cys Gly Val Val	
20 25 30	
TTC ATC GTC TAC TCG GAG AGC AAA ATG GTC ATT GTG TGC CTC ATC ACC	144
Phe Ile Val Tyr Ser Glu Ser Lys Met Val Ile Val Cys Leu Ile Thr	
35 40 45	
ATG TTC TTC GCC ATG ATG CTC CTC ATG GGC ACC CTC TAC GTG CAC ATG	192
Met Phe Phe Ala Met Met Leu Leu Met Gly Thr Leu Tyr Val His Met	
50 55 60	
TTC CTC TTT GCG CGG CTG CAC GTC AAG CGC ATA GCA GCA CTG CCA CCT	240
Phe Leu Phe Ala Arg Leu His Val Lys Arg Ile Ala Ala Leu Pro Pro	
65 70 75 80	
GCC GAC GGG GTG GCC CCA CAG CAA CAC TCA TGC ATG AAG GGG GCA GTC	288
Ala Asp Gly Val Ala Pro Gln Gln His Ser Cys Met Lys Gly Ala Val	
85 90 95	
ACC CTC ACC ATC CTG CTG GGC ATT	312
Thr Leu Thr Ile Leu Leu Gly Ile	
100	

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Tyr Ala Leu Arg Tyr His Ser Ile Val Thr Val Arg Arg Ala Leu	
1 5 10 15	
Thr Leu Ile Val Ala Ile Trp Val Cys Cys Gly Val Cys Gly Val Val	
20 25 30	
Phe Ile Val Tyr Ser Glu Ser Lys Met Val Ile Val Cys Leu Ile Thr	
35 40 45	

103

Met Phe Phe Ala Met Met Leu Leu Met Gly Thr Leu Tyr Val His Met
 50 55 60

Phe Leu Phe Ala Arg Leu His Val Lys Arg Ile Ala Ala Leu Pro Pro
 65 70 75 80

Ala Asp Gly Val Ala Pro Gln Gln His Ser Cys Met Lys Gly Ala Val
 85 90 95

Thr Leu Thr Ile Leu Leu Gly Ile
 100

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (PCR-fragment)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CTG TGT GTG ATC GCG CTG GAC CGG TAC ATC TCC ATC TTC TAC GCA CTG	48
Leu Cys Val Ile Ala Leu Asp Arg Tyr Ile Ser Ile Phe Tyr Ala Leu	
1 5 10 15	
CGC TAC CAC AGC ATC GTG ACC CTG CCG CGG GCG CCG GAA GCC GTT GCG	96
Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Pro Glu Ala Val Ala	
20 25 30	
GCC ATC TGG GTG GCC AGT GTC GTC TTC AGC ACG CTC TTC ATC GCC TAC	144
Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe Ile Ala Tyr	
35 40 45	
TAC GAC CAC GTG GCC GTC CTG CTG TGC CTC GTG GTC TTC TTC CTG GCT	192
Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe Phe Leu Ala	
50 55 60	
ATG CTG GTG CTC ATG GCC GTG CTG TAC GTC CAC ATG CTG GCC CGG GCC	240
Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu Ala Arg Ala	
65 70 75 80	
TGC CAG CAC GCC CAG GGC ATC GCC CGG CTC CAC AAG AGG CAG CGC CCG	288
Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg Gln Arg Pro	
85 90 95	
GTC CAC CAG GGC TTT GGC CTT AAA GGC GCT GTC ACC CTC ACC ATC CTG	336
Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr Ile Leu	
100 105 110	

104

CTG GGC ATT TTC ACC GTC TCG TGG CGC CCC TTC TTC
 Leu Gly Ile Phe Thr Val Ser Trp Arg Pro Phe Phe
 115 120

372

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Leu Cys Val Ile Ala Leu Asp Arg Tyr Ile Ser Ile Phe Tyr Ala Leu
 1 5 10 15
 Arg Tyr His Ser Ile Val Thr Leu Pro Arg Ala Pro Glu Ala Val Ala
 20 25 30
 Ala Ile Trp Val Ala Ser Val Val Phe Ser Thr Leu Phe Ile Ala Tyr
 35 40 45
 Tyr Asp His Val Ala Val Leu Leu Cys Leu Val Val Phe Phe Leu Ala
 50 55 60
 Met Leu Val Leu Met Ala Val Leu Tyr Val His Met Leu Ala Arg Ala
 65 70 75 80
 Cys Gln His Ala Gln Gly Ile Ala Arg Leu His Lys Arg Gln Arg Pro
 85 90 95
 Val His Gln Gly Phe Gly Leu Lys Gly Ala Val Thr Leu Thr Ile Leu
 100 105 110
 Leu Gly Ile Phe Thr Val Ser Trp Arg Pro Phe Phe
 115 120

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGGAATTCTA CGCACTGCGC TACCACAGCA TCGTG

35

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGGGATCCAA TGCCCAGCAG GATGGTGAGG GTGA

34

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (cDNA)

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 616..1590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTTGAGGAGA ATGTCGTGCA GTAGCCTTAG GAATGTGAAC ATTGGGAGAC TGGCTGGGAT 60
TTTGTAGGTT ATGAGAAGGG GACACTTATG ATATGTGAAC TTGAGCCCAG GAGAGAAGCC 120
ATAAAAAGTG AAAGTGTCTT GGGCACTTGG AGGTGAGTGT CTCTCTAGTA AGATGCATGT 180
GAAAGGCCTG GGAGCTGAAA GCAAGCAGAG CAGAAGAGGC TGGTGAAGAT TCTAATCTGC 240
GTGTCCAGGG GCACTCTTCC AGGTCTCAGG AACGCAGGTC AGAATGTGCA AGCCAGCTGC 300
CGGGCACGTG GCTCACCCTT GTAGTACCAG CACTTTGGGA GGCTGAGAGA GAAGATCGCT 360
TGTGGCCAGG AGTTTGAGAC CAGACTGGGG CTTCATAGGG AGACCCTGTC TCTTAAAAAA 420
AAAAAAAAAA AAGGACTGAG TGAGCCGAGC CCAGTCCTCT CATGCACTGT GTCATTCATC 480
CCCTTTCTTA GGCTGTGTTG GTTCTAGGCT AGCTGCTGTC TTTCTTTGGT AGGCTGCTAA 540
CCTCTTTGGA TTGTGAATTT AAAACATGTT TTACAGTAAA TTTGCTGCCA AGACAAGAGG 600
TGTATTTCTC CAGCA ATG AAT TCC TCA TTT CAC CTG CAT TTC TTG GAT CTC 651
Met Asn Ser Ser Phe His Leu His Phe Leu Asp Leu
1 5 10
AAC CTG AAT GCC ACA GAG GGC AAC CTT TCA GGA CCC AAT GTC AAA AAC 699
Asn Leu Asn Ala Thr Glu Gly Asn Leu Ser Gly Pro Asn Val Lys Asn
15 20 25

106

AAG TCT TCA CCA TGT GAA GAC ATG GGC ATT GCT GTG GAG GTG TTT CTC	747
Lys Ser Ser Pro Cys Glu Asp Met Gly Ile Ala Val Glu Val Phe Leu	
30 35 40	
ACT CTG GGT GTC ATC AGC CTC TTG GAG AAC ATC TTG GTC ATA GGG GCC	795
Thr Leu Gly Val Ile Ser Leu Leu Glu Asn Ile Leu Val Ile Gly Ala	
45 50 55 60	
ATA GTG AAG AAC AAA AAC CTG CAC TCC CCC ATG TAC TTC TTC GTG TGC	843
Ile Val Lys Asn Lys Asn Leu His Ser Pro Met Tyr Phe Phe Val Cys	
65 70 75	
AGC CTG GCA GTG GCG GAC ATG CTG GTG AGC ATG TCC AGT GCC TGG GAG	891
Ser Leu Ala Val Ala Asp Met Leu Val Ser Met Ser Ser Ala Trp Glu	
80 85 90	
ACC ATC ACC ATC TAC CTA CTC AAC AAC AAG CAC CTA GTG ATA GCA GAC	939
Thr Ile Thr Ile Tyr Leu Leu Asn Asn Lys His Leu Val Ile Ala Asp	
95 100 105	
GCC TTT GTG CGC CAC ATT GAC AAT GTG TTT GAC TCC ATG ATC TGC ATT	987
Ala Phe Val Arg His Ile Asp Asn Val Phe Asp Ser Met Ile Cys Ile	
110 115 120	
TCC GTG GTG GCA TCC ATG TGC AGC TTA CTG GCC ATT GCA GTG GAT AGG	1035
Ser Val Val Ala Ser Met Cys Ser Leu Leu Ala Ile Ala Val Asp Arg	
125 130 135 140	
TAC GTC ACC ATC TTC TAC GCC CTG CGC TAC CAC CAC ATC ATG ACG GCG	1083
Tyr Val Thr Ile Phe Tyr Ala Leu Arg Tyr His His Ile Met Thr Ala	
145 150 155	
AGG CGC TCA GGG GCC ATC ATC GCC GGC ATC TGG GCT TTC TGC ACG GGC	1131
Arg Arg Ser Gly Ala Ile Ile Ala Gly Ile Trp Ala Phe Cys Thr Gly	
160 165 170	
TGC GGC ATT GTC TTC ATC CTG TAC TCA GAA TCC ACC TAC GTC ATC CTG	1179
Cys Gly Ile Val Phe Ile Leu Tyr Ser Glu Ser Thr Tyr Val Ile Leu	
175 180 185	
TGC CTC ATC TCC ATG TTC TTC GCT ATG CTG TTC CTC CTG GTG TCT CTG	1227
Cys Leu Ile Ser Met Phe Phe Ala Met Leu Phe Leu Leu Val Ser Leu	
190 195 200	
TAC ATA CAC ATG TTC CTC CTG GCG CGG ACT CAC GTC AAG CGG ATC GCG	1275
Tyr Ile His Met Phe Leu Leu Ala Arg Thr His Val Lys Arg Ile Ala	
205 210 215 220	
CTC TGC CCG GGG CCA GCT CTG CGC GGC AGA GGA CCA GCA TGG CAG GGC	1323
Leu Cys Pro Gly Pro Ala Leu Arg Gly Arg Gly Pro Ala Trp Gln Gly	
225 230 235	
GCG GTC ACC GTC ACC ATG CTG CTG GGC GTG TTT ACC GTG TGC TGG GCC	1371
Ala Val Thr Val Thr Met Leu Leu Gly Val Phe Thr Val Cys Trp Ala	
240 245 250	

107

CCG TTC TTC CTT CAT CTC ACT TTA ATG CTT TCT TGC CCT CAG AAC CTC 1419
 Pro Phe Phe Leu His Leu Thr Leu Met Leu Ser Cys Pro Gln Asn Leu
 255 260 265

TAC TGC TCT CGC TTC ATG TCT CAC TTC AAT ATG TAC CTC ATA CTC ATC 1467
 Tyr Cys Ser Arg Phe Met Ser His Phe Asn Met Tyr Leu Ile Leu Ile
 270 275 280

ATG TGT AAT TCC GTG ATG GAC CCT CTC ATA TAT GCC TTC CGC AGC CAA 1515
 Met Cys Asn Ser Val Met Asp Pro Leu Ile Tyr Ala Phe Arg Ser Gln
 285 290 295 300

GAG ATG CGG AAG ACC TTT AAG GAG ATT ATT TGC TGC CGT GGT TTC AGG 1563
 Glu Met Arg Lys Thr Phe Lys Glu Ile Ile Cys Cys Arg Gly Phe Arg
 305 310 315

ATC GCC TGC AGC TTT CCC AGA AGG GAT TAACGACAAA GTGCTCCTCT 1610
 Ile Ala Cys Ser Phe Pro Arg Arg Asp
 320 325

CTGTGGCTCT GTTCTCCTTT GTTTGCTCAC CTATGACAAA 1650

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Met Asn Ser Ser Phe His Leu His Phe Leu Asp Leu Asn Leu Asn Ala
 1 5 10 15

Thr Glu Gly Asn Leu Ser Gly Pro Asn Val Lys Asn Lys Ser Ser Pro
 20 25 30

Cys Glu Asp Met Gly Ile Ala Val Glu Val Phe Leu Thr Leu Gly Val
 35 40 45

Ile Ser Leu Leu Glu Asn Ile Leu Val Ile Gly Ala Ile Val Lys Asn
 50 55 60

Lys Asn Leu His Ser Pro Met Tyr Phe Phe Val Cys Ser Leu Ala Val
 65 70 75 80

Ala Asp Met Leu Val Ser Met Ser Ser Ala Trp Glu Thr Ile Thr Ile
 85 90 95

Tyr Leu Leu Asn Asn Lys His Leu Val Ile Ala Asp Ala Phe Val Arg
 100 105 110

His Ile Asp Asn Val Phe Asp Ser Met Ile Cys Ile Ser Val Val Ala
 115 120 125

108

Ser Met Cys Ser Leu Leu Ala Ile Ala Val Asp Arg Tyr Val Thr Ile
 130 135 140

Phe Tyr Ala Leu Arg Tyr His His Ile Met Thr Ala Arg Arg Ser Gly
 145 150 155 160

Ala Ile Ile Ala Gly Ile Trp Ala Phe Cys Thr Gly Cys Gly Ile Val
 165 170 175

Phe Ile Leu Tyr Ser Glu Ser Thr Tyr Val Ile Leu Cys Leu Ile Ser
 180 185 190

Met Phe Phe Ala Met Leu Phe Leu Leu Val Ser Leu Tyr Ile His Met
 195 200 205

Phe Leu Leu Ala Arg Thr His Val Lys Arg Ile Ala Leu Cys Pro Gly
 210 215 220

Pro Ala Leu Arg Gly Arg Gly Pro Ala Trp Gln Gly Ala Val Thr Val
 225 230 235 240

Thr Met Leu Leu Gly Val Phe Thr Val Cys Trp Ala Pro Phe Phe Leu
 245 250 255

His Leu Thr Leu Met Leu Ser Cys Pro Gln Asn Leu Tyr Cys Ser Arg
 260 265 270

Phe Met Ser His Phe Asn Met Tyr Leu Ile Leu Ile Met Cys Asn Ser
 275 280 285

Val Met Asp Pro Leu Ile Tyr Ala Phe Arg Ser Gln Glu Met Arg Lys
 290 295 300

Thr Phe Lys Glu Ile Ile Cys Cys Arg Gly Phe Arg Ile Ala Cys Ser
 305 310 315 320

Phe Pro Arg Arg Asp
 325

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO 17:

GGAAGCTTTC TTTGGTAGGC TG

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GGTCTAGAGC CACAGAGAGG AG

22

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CTGCATTCT TGGATCT

17

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AAGCTGCACA TGGATGC

17